WHAT IS CLAIMED IS:

1. An isolated polypeptide selected from the group consisting of SEQ ID NOs: 2, 4, and 6, and the fragments comprising the amino acid residues 112 to 119 of SEQ ID NO: 6.

2. An isolated nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 3 and 5, and fragments thereof.

3. The isolated nucleic acid of Claim 2, wherein the fragments comprise nucleotides 196 to 201 of SEQ ID NO: 1.

4. The isolated nucleic acid of Claim 2, wherein the fragments comprise nucleotides 486 to 491 of SEQ ID NO: 3.

5. The isolated nucleic acid of Claim 2, wherein the fragments comprise nucleotides 915 to 920 of SEQ ID NO: 5.

6. An expression vector comprising the nucleic acid of Claim2.

7. A host cell transformed with the expression vector of Claim 6.

8. A method for producing the polypeptide of Claim 1, which comprises the steps of:

(1) culturing the host cell of Claim 7 under a condition suitable for the expression of the polypeptide; and

(2) recovering the polypeptide from the host cell culture.

9. An antibody specifically binding to the polypeptide of Claim 1.

10. A method for diagnosing the diseases associated with the deficiency of the SACH gene in a mammal, in particular cancers, which comprises detecting the nucleic acid of Claim 2 or the polypeptide of Claim

1.

11. The method of Claim 10, wherein the detection of the nucleic acid of Claim 2 comprises the steps of:

(1) extracting the total RNA from a sample obtained from the mammal;

(2) amplifying the RNA by reverse transcriptase-polymerase chain reaction (RT-PCR) to obtain a cDNA sample;

(3) bringing the cDNA sample into contact with the nucleic acid of Claim 2; and

(4) detecting whether the cDNA hybridizes with the nucleic acid of Claim 2.

12. The method of Claim 11 further comprising the step of determining the amount of the hybridized sample.

13. The method of Claim 10, wherein the detection of the nucleic acid of Claim 2 comprises the steps of:

(1) extracting the total RNAs of cells obtained from the mammal;

(2) amplifying the RNA by reverse transcriptase-polymerase chain reaction (RT-PCR) with a set of primers to obtain a cDNA comprising the fragments comprising nucleotides 196 to 201 of SEQ ID NO: 1 or nucleotides 486 to 491 of SEQ ID NO: 3 or nucleotides 915 to 920 of SEQ ID NO: 5; and

(3) detecting whether the cDNA is obtained.

14. The method of Claim 13, wherein the forward primer has a sequence comprising the nucleotides 196 to 201 of SEQ ID NO: 1 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 1 at any other locations downstream of nucleotide 201, or alternatively, the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 1 containing nucleotides 196 to 201 and the

forward primer has a sequence comprising the nucleotides of SEQ ID NO: 1 at any other locations upstream of nucleotide 196.

15. The method of Claim 13, wherein the forward primer has a sequence comprising the nucleotides 486 to 491 of SEQ ID NO: 3 and the reverse primer has a sequence complementary to the sequence complementary to the nucleotides of SEQ ID NO: 3 at any other locations downstream of nucleotide 491, or alternatively, the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 3 containing nucleotides 486 to 491 and the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 3 at any other locations upstream of nucleotide 486.

16. The method of Claim 13, wherein the forward primer has a sequence comprising the nucleotides between 915 to 920 of SEQ ID NO: 5 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 5 at any other locations downstream of nucleotide 920, or alternatively, the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 5 containing nucleotides between 915 to 920 and the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 5 at any other locations upstream of nucleotide 915.

17. The method of Claim 13, wherein the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 1 at any other locations upstream of nucleotide 196 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 1 at any other locations downstream of nucleotide 201.

18. The method of Claim 13, wherein the forward primer has a sequence comprising the nucleotides of SEQ ID NO: 3 at any other locations upstream of nucleotide 486 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 3 at any other locations downstream of nucleotide 491.

19. The method of Claim 13, wherein the forward primer has a sequence the nucleotides of SEQ ID NO: 5 at any other locations upstream of nucleotide 915 and the reverse primer has a sequence complementary to the nucleotides of SEQ ID NO: 5 at any other locations downstream of nucleotide 920.

20. The method of Claim 17, wherein the cDNA sample amplified from SEQ ID NO: 1 is 512bp shorter than that from SACH.

21. The method of Claim 18, wherein the cDNA sample amplified from SEQ ID NO: 3 is 478bp shorter than that from SACH.

22. The method of Claim 19, wherein the cDNA sample amplified from SEQ ID NO: 5 is 168bp shorter than that from SACH.

23. The method of Claim 13 further comprising the step of detecting the amount of the amplified cDNA sample.

24. The method of Claim 10, wherein the detection of the polypeptide of Claim 1 comprises the steps of contacting the antibody of Claim 9 with protein samples extracted from the mammal, and detecting whether an antibody-polypeptide complex is formed.

25. The method of Claim 24 further comprising the step of determining the amount of the antibody-polypeptide complex.